

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 20, 2005, 07:01:25 ; Search time 42 Seconds
(without alignments)
26.660 Million cell updates/sec

Title: US-10-679-081-2

Perfect score: 97
Sequence: 1 FKADEKKFWGKYLE 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2.6/prodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2.6/prodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2.6/prodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2.6/prodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2.6/prodata/1/iaa/PCUS COMB.pcp.*
- 6: /cgn2.6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	18	3	US-08-477-928A-11
2	87	100.0	582	1	US-08-134-638-1
3	87	100.0	583	1	US-08-448-196A-4
4	87	100.0	583	1	US-08-448-196A-6
5	81	93.1	18	3	US-08-477-928A-12
6	75	86.2	14	3	US-08-477-928A-42
7	59	67.8	12	3	US-08-477-928A-15
8	56	64.4	12	3	US-08-477-928A-13
9	53	60.9	10	3	US-08-477-928A-16
10	53	60.9	583	1	US-08-448-196A-5
11	45	51.7	233	4	US-09-599-360B-85
12	44	50.6	59	4	US-09-663-600A-182
13	44	50.6	63	4	US-09-663-600A-88
14	41	47.1	311	4	US-09-107-532A-4970
15	40	46.0	332	4	US-09-107-532A-7060
16	40	46.0	376	4	US-09-134-000C-6024
17	40	46.0	391	4	US-09-134-000C-6210
18	40	46.0	590	1	US-08-448-196A-9
19	39	44.8	156	4	US-09-270-767-40593
20	39	44.8	156	4	US-09-270-767-55809
21	39	44.8	168	2	US-08-667-023-2
22	39	44.8	168	3	US-08-713-825-3
23	39	44.8	168	3	US-09-199-842-3
24	39	44.8	168	4	US-09-460-532-3
25	39	44.8	223	2	US-08-869-793-6
26	39	44.8	226	4	US-09-134-000C-5879
27	39	44.8	226	4	US-09-270-767-44619

28	39	44.8	340	4	US-09-902-540-11410	Sequence 11410, A
29	39	44.8	481	4	US-09-949-016-6826	Sequence 6826, Ap
30	39	44.8	486	4	US-09-949-016-8176	Sequence 8176, Ap
31	39	44.8	509	3	US-08-845-548-2	Sequence 2, Appl
32	39	44.8	517	1	US-08-190-802A-30	Sequence 30, Appl
33	39	44.8	517	3	US-08-477-346-30	Sequence 30, Appl
34	39	44.8	517	3	US-08-473-089-30	Sequence 30, Appl
35	39	44.8	517	4	US-08-487-072A-30	Sequence 30, Appl
36	39	44.8	569	4	US-09-832-161-18	Sequence 18, Appl
37	39	44.8	569	4	US-09-385-219A-2	Sequence 2, Appl
38	39	44.8	569	4	US-09-601-168B-2	Sequence 2, Appl
39	39	44.8	585	1	US-08-153-799-14	Sequence 14, Appl
40	39	44.8	585	1	US-08-448-196A-3	Sequence 3, Appl
41	39	44.8	585	2	US-08-984-176-1	Sequence 1, Appl
42	39	44.8	585	2	US-08-702-572-2	Sequence 2, Appl
43	39	44.8	585	3	US-08-769-746-2	Sequence 2, Appl
44	39	44.8	609	1	US-08-222-613-3	Sequence 3, Appl
45	39	44.8	609	1	US-08-433-037-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-477-928A-11
; Sequence 11, Application US/08477928A
; Patent No. 6207389
; GENERAL INFORMATION:
; APPLICANT: Dosch, Hans M.
; TITLE OF INVENTION: METHODS FOR CONTROLLING T
; TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESS: BAKER & BOTTS
; STREET: 1299 Pennsylvania Avenue
; CITY: Washington D.C.
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,928A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36902
; REFERENCE/DOCKET NUMBER: 19060-0105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 639 7700
; TELEFAX: (202) 639 7890
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-928A-11

Query Match 100.0%; Score 87; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FKADEKKFWGKYLE 15
Db 1 FKADEKKFWGKYLE 15